

SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha
<120> Immunochemical Assay Method for Anti-HM 24 Antibody
<130> F943
<150> JP 10-060613
<151> 1998-03-20
<160> 29
<210> 1
<211> 399
<212> DNA
<213> Homosapiens
<223> Nucleotide sequence of extracellular domain of soluble
HM 1.24 antigenic protein

<400> 1
aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc 48
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
1 5 10 15
aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
20 25 30
ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
35 40 45
gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
50 55 60
gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 240
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
65 70 75 80
gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
85 90 95
agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
100 105 110

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agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc      384
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
      115              120              125

gct ctg ctg cag tga      399
Ala Leu Leu Gln
      130
<210> 2
<211> 510
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223> Nucleotide sequence coding for a fusion protein
      comprising leader sequence, FLAG peptide and soluble
      HM 1.24 antigenic protein
<400> 2
gaattccac c atg gga tgg agc tgt atc atc ctc ttc ttg gta gca      47
      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala
      1              5              10

aca gct aca ggt gtc cac tcc gac tac aaa gac gat gac gat aaa ggt      95
Thr Ala Thr Gly Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gly
      15              20              25

acc aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt      143
Thr Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys
      30              35              40

cgc aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag      191
Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys
      45              50              55              60

ggc ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg      239
Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val
      65              70              75

atg gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag      287
Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys
      80              85              90

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aaa gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt      335
Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu
      95                      100                      105

cag gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc      383
Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val
      110                      115                      120

tta agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac      431
Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp
      125                      130                      135                      140

tcc agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc      479
Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu
      145                      150                      155

agc gct ctg ctg cag tgagatccca ggatcc                                510
Ser Ala Leu Leu Gln
      160

<210> 3
<211> 445
<212> DNA
<213> Artificial Sequence
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<223> Nucleotide sequence coding for a fusion protein
      comprising HA peptide and soluble HM 1.24 antigenic
      protein

<400> 3
tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc      48
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
      1                      5                      10                      15

cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc      96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
      20                      25                      30

ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag      144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
      35                      40                      45

gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc      192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
      50                      55                      60

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ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag 240
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80
 gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag 288
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95
 gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg 336
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110
 gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg 384
 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala
 115 120 125
 ccc cag ctg ctg att gtg ctg ctg ggc ctc agc gct ctg ctg cag 429
 Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
 130 135 140
 tgagatccca ggatcc 445
 <210> 4
 <211> 387
 <212> DNA
 <213> Artificial Sequence
 <223> Nucleotide sequence coding for a fusion protein
 comprising HA peptide and C-terminal-lacking soluble
 HM 1.24 antigenic protein
 <400> 4
 tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc 48
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15
 cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc 96
 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30
 ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag 144
 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45
 gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc 192
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60

ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag	240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu	
65 70 75 80	
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag	288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu	
85 90 95	
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg	336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala	
100 105 110	
gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct	378
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala	
115 120 125	
tgaggatcc	387
<210> 5	
<211> 85	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Nucleotide sequence coding for HA peptide	
<400> 5	
ctctggctcc caggtgcacg atgtgca tac cca tac gac gtc cca gac tac	51
Tyr Pro Tyr Asp Val Pro Asp Tyr	
1 5	
gct ggtaccaagg tggaaatcaa acgtacggaa t	85
Ala	
<210> 6	
<211> 535	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Nucleotide sequence coding for CG M/HA-HM164	
<400> 6	
agatctctca cc atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg	48
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu	
1 5 10	

ctc tgg ctc cca ggt gca cga tgt gca tac cca tac gac gtc cca gac	96
Leu Trp Leu Pro Gly Ala Arg Cys Ala Tyr Pro Tyr Asp Val Pro Asp	
15 20 25	
tac gct ggt acc aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg	144
Tyr Ala Gly Thr Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val	
30 35 40	
atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg acc gag	192
Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu	
45 50 55 60	
gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac	240
Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn	
65 70 75	
cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag gcc caa	288
His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln	
80 85 90	
gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca tta aac	336
Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn	
95 100 105	
cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga aga gaa	384
His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu	
110 115 120	
aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac ccc agc	432
Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser	
125 130 135 140	
tcc cag gac tcc agc tcc gct tgaggatcct atggttacca actacctaga	483
Ser Gln Asp Ser Ser Ser Ala	
145	
ctggattcgt gacaacatgc ggccgtgata totacgtatg atcagcctcg ac	535
<210> 7	
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<213> Artificial Sequence	
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<210> 8	

<211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 8
 atcgccctgga gacgccatca 20
 <210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 9
 taaaggtacc aacagcgagg cctgccg 27
 <210> 10
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 10
 ctgctgcagt gagatcccag gatccata 28
 <210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 11
 caggactcca gctccgcttg aggatcctat 30
 <210> 12
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA comprising leader sequence and FLAG
 coding sequence
 <400> 12
 aattcccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60
 ccactccgac taaaagacg atgaagataa aggtaccgcg gccgcg 106
 <210> 13
 <211> 106
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA comprising leader sequence and FLAG
 coding sequence
 <400> 13
 gatccgcggc cgcggtacct ttatcgatcat cgtctttgta gtcggagtgg acacctgtag 60
 ctgttgctac caagaagagg atgatacagc tccatcccat ggtggg 106
 <210> 14
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA coding for HA peptide
 <400> 14
 gtgcataccc atacgacgtc ccagactacg ctggtac 37
 <210> 15
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA coding for HA peptide
 <400> 15
 cagcgtagtc tgggacgctg tatgggtatg cacatc 36
 <210> 16
 <211> 1014
 <212> DNA

<213> Homosapiens

<223> Nucleotide sequence coding for humam HM 1.24 antigenic protein expressed on cell membrane

<400> 16

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gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc      49
                               Met Ala Ser Thr Ser Tyr Asp Tyr Cys
                               1           5

aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg      97
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10           15           20           25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg      145
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
 30           35           40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt      193
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
 45           50           55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag      241
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
 60           65           70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc      289
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
 75           80           85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag      337
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
 90           95          100          105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act      385
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
 110          115          120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg      433
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
 125          130          135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac      481
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
 140          145          150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg      529
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
 155          160          165
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att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 582
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170                      175                      180
acatcttgga aggtccgtcc tgetcggett ttcgcttgaa cattcccttg atctcatcag 642
ttctgagcgg gtcattggggc aacacgggta gcggggagag cacggggtag ccggagaagg 702
gcctctggag caggtctgga gggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 762
ttgaccacagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 822
tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 882
ggtttttttt gcgggggggg ttgctttttt ctgggggtctt tgagctccaa aaaaataaac 942
acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 1002
gggcggccgc ca 1014
<210> 17
<211> 379
<212> DNA
<213> Artificial Sequence
<220>
<223> Nucleotide sequence coding for L chain V region
        version a of humamized anti-HM 1.24 antibody
<400> 17
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Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
        -15                      -10                      -5
gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
        -1  1                      5                      10
agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
        15                      20                      25
aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        30                      35                      40                      45
ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 240
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
        50                      55                      60
ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
        65                      70                      75

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ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 336
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
 80 85 90
 act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c 379
 Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 95 100 105
 <210> 18
 <211> 418
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Nucleotide sequence coding for H chain V region
 version r of humanized anti-HM 1.24 antibody
 <400> 18
 atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
 -15 -10 -5
 gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 -1 1 5 10
 cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
 act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
 50 55 60
 cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288
 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
 65 70 75
 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac	384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr	
95 100 105	
tgg ggg caa ggg acc acg gtc acc gtc tcc tca g	418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
110 115 120	
<210> 19	
<211> 418	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Nucleotide sequence coding for H chain V region	
version s of humanized anti-HM 1.24 antibody	
<400> 19	
atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt	48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	
-15 -10 -5	
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt	192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt	240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser	
50 55 60	
cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc	288
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser	
65 70 75	
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
 95 100 105

tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 110 115 120

<210> 20

<211> 132

<212> PRT

<213> Homosapiens

<223> Amino acid sequence of soluble HM 1.24 antigenic
 protein

<400> 20

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 1 5 10 15

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 20 25 30

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 35 40 45

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 50 55 60

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 115 120 125

Ala Leu Leu Gln
 130

<210> 21

<211> 161

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising
leader sequence, FLAG peptide and soluble HM 1.24
antigenic protein

<400> 21

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1               5               10               15
Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Asn Ser Glu
              20              25              30
Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr
              35              40              45
His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp
              50              55              60
Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met
              65              70              75              80
Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu
              85              90              95
Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser
              100             105             110
Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg
              115             120             125
Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
              130             135             140
Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu
              145             150             155             160
Gln

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<210> 22

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising HA
peptide and soluble HM 1.24 antigenic protein

<400> 22

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
  1               5               10               15
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
              20              25              30

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Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110
 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala
 115 120 125
 Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
 130 135 140

<210> 23

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising HA
 peptide and C-terminal lacking soluble HM 1.24
 antigenic protein

<400> 23

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15
 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30
 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
115 120 125

<210> 24

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HA peptide

<400> 24

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 25

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of CGM/HA-HM164

<400> 25

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu pro

1 5 10 15

Gly Ala Arg Cys Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr

20 25 30

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

35 40 45

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

50 55 60

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

65 70 75 80

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

85 90 95

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

100 105 110

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

115 120 125

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

130 135 140

44710	44711	44712	44713	44714	44715	44716	44717	44718	44719	44720	44721	44722	44723	44724	44725	44726	44727	44728	44729	44730	44731	44732	44733	44734	44735	44736	44737	44738	44739	44740	44741	44742	44743	44744	44745	44746	44747	44748	44749	44750	44751	44752	44753	44754	44755	44756	44757	44758	44759	44760	44761	44762	44763	44764	44765	44766	44767	44768	44769	44770	44771	44772	44773	44774	44775	44776	44777	44778	44779	44780	44781	44782	44783	44784	44785	44786	44787	44788	44789	44790	44791	44792	44793	44794	44795	44796	44797	44798	44799	44800	44801	44802	44803	44804	44805	44806	44807	44808	44809	44810	44811	44812	44813	44814	44815	44816	44817	44818	44819	44820	44821	44822	44823	44824	44825	44826	44827	44828	44829	44830	44831	44832	44833	44834	44835	44836	44837	44838	44839	44840	44841	44842	44843	44844	44845	44846	44847	44848	44849	44850	44851	44852	44853	44854	44855	44856	44857	44858	44859	44860	44861	44862	44863	44864	44865	44866	44867	44868	44869	44870	44871	44872	44873	44874	44875	44876	44877	44878	44879	44880	44881	44882	44883	44884	44885	44886	44887	44888	44889	44890	44891	44892	44893	44894	44895	44896	44897	44898	44899	44900	44901	44902	44903	44904	44905	44906	44907	44908	44909	44910	44911	44912	44913	44914	44915	44916	44917	44918	44919	44920	44921	44922	44923	44924	44925	44926	44927	44928	44929	44930	44931	44932	44933	44934	44935	44936	44937	44938	44939	44940	44941	44942	44943	44944	44945	44946	44947	44948	44949	44950	44951	44952	44953	44954	44955	44956	44957	44958	44959	44960	44961	44962	44963	44964	44965	44966	44967	44968	44969	44970	44971	44972	44973	44974	44975	44976	44977	44978	44979	44980	44981	44982	44983	44984	44985	44986	44987	44988	44989	44990	44991	44992	44993	44994	44995	44996	44997	44998	44999	45000
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<220>

<223> Amino acid sequence of L chain V region version a of
humanized amti-HM 1.24 antibody

<400> 27

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Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
      -15                -10                -5
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
      -1  1                5                10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
      15                20                25
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
      30                35                40                45
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
      50                55                60
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
      65                70                75
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
      80                85                90
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      95                100                105
```

<210> 28

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version r of
humanized anti-HM 1.24 antibody

<400> 28

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Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
      -15                -10                -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      -1  1                5                10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                20                25
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30                35                40                45
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Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
 50 55 60
 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
 65 70 75
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
 95 100 105
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 110 115 120

<210> 29

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version s of
humanized anti-HM 1.24 antibody

<400> 29

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
 -15 -10 -5
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 -1 1 5 10
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
 50 55 60
 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
 65 70 75
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
 95 100 105
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 110 115 120